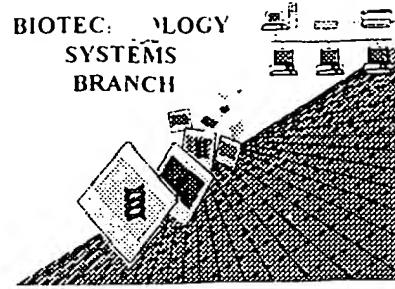


0280

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/759,130

Source: OIPE

Date Processed by STIC: 1-29-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/759,130

- ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
- 1 Wrapped Nucleic The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: MCCARTHY, Sean A
 4 FRASER, Christopher C
 5 SHARP, John D
 6 BARNES, Thomas S
 7 KIRST, Susan J
 8 MACKAY, Charles R
 9 MYERS, Paul S
 10 LEIBY, Kevin R
 11 WRIGHTON, Nicholas
 12 GOODEARL, Andrew
 13 HOLTZMAN, Douglas A
 15 <120> TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC,
 16 DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER USES
 18 <130> FILE REFERENCE: 210147.0066/66US
 C--> 20 <140> CURRENT APPLICATION NUMBER: US/09/759,130
 21 <141> CURRENT FILING DATE: 2001-01-12
 23 <150> PRIOR APPLICATION NUMBER: US 09/479,249
 24 <151> PRIOR FILING DATE: 2000-01-07
 26 <150> PRIOR APPLICATION NUMBER: US 09/559,497
 27 <151> PRIOR FILING DATE: 2000-04-27
 29 <150> PRTOR APPLICATION NUMBER: US 09/578,063
 30 <151> PRTOR FILING DATE: 2000-05-24
 32 <150> PRTOR APPLICATION NUMBER: US 09/333,159
 33 <151> PRTOR FILING DATE: 1999-06-14
 35 <150> PRTOR APPLICATION NUMBER: US 09/596,194
 36 <151> PRTOR FILING DATE: 2000-07-14
 38 <150> PRTOR APPLICATION NUMBER: US 09/342,364
 39 <151> PRTOR FILING DATE: 1999-06-29
 41 <150> PRTOR APPLICATION NUMBER: US 09/608,452
 42 <151> PRTOR FILING DATE: 2000-06-30
 44 <150> PRTOR APPLICATION NUMBER: US 09/393,996
 45 <151> PRTOR FILING DATE: 1999-09-10
 47 <150> PRTOR APPLICATION NUMBER: US 09/602,871
 48 <151> PRTOR FILING DATE: 2000-06-23
 50 <150> PRTOR APPLICATION NUMBER: US 09/420,707
 51 <151> PRTOR FILING DATE: 1999-10-19
 53 <160> NUMBER OF SEQ ID NOS: 460
 55 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

216 <210> SEQ ID NO. 3
 217 <211> LENGTH: 1151
 218 <212> TYPE: PRF
 219 <213> ORGANISM: HOMO sapiens
 221 <400> SEQUENCE: 3

Number of amino acids differ:
 -1151 listed
 911 shown

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
TIME: 13:45:10

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

222 Met His Gln Met Asn Ala Lys Met His Phe Arg Phe Val Phe Ala Leu
223 1 5 10 15
225 Leu Ile Val Ser Phe Asn His Asp Val Leu Gly Lys Asn Leu Lys Tyr
226 20 25 30
228 Arg Ile Tyr Glu Glu Gln Arg Val Gly Ser Val Ile Ala Arg Leu Ser
229 35 40 45
231 Glu Asp Val Ala Asp Val Leu Leu Lys Leu Pro Asn Pro Ser Thr Val
232 50 55 60
234 Arg Phe Arg Ala Met Gln Arg Gly Asn Ser Pro Leu Leu Val Val Asn
235 65 70 75 80
237 Glu Asp Asn Gly Glu Ile Ser Ile Gly Ala Thr Ile Asp Arg Glu Gln
238 85 90 95
240 Thr Leu Pro Thr Glu His Leu Gln Leu Phe His Ile Glu Val Glu Val
241 100 105 110
243 Leu Asp Ile Asn Asp Asn Ser Pro Gln Phe Ser Arg Ser Leu Ile Pro
244 115 120 125
246 Ile Glu Ile Ser Glu Ser Ala Ala Val Gly Thr Arg Ile Pro Leu Asp
247 130 135 140
249 Ser Ala Phe Asp Pro Asp Val Gly Glu Asn Ser Leu His Thr Tyr Ser
250 145 150 155 160
252 Leu Ser Ala Asn Asp Phe Phe Asn Ile Glu Val Arg Thr Arg Thr Asp
253 165 170 175
255 Glu Leu Lys Ser Ser Tyr Glu Leu Gln Leu Thr Ala Ser Asp Met Gly
256 180 185 190
258 Val Pro Gln Arg Ser Gly Ser Ser Ile Leu Lys Ile Ser Ile Ser Asp
259 195 200 205
261 Ser Asn Asp Asn Ser Pro Ala Phe Glu Gln Gln Ser Tyr Ile Ile Gln
262 210 215 220
264 Leu Leu Glu Asn Ser Pro Val Gly Thr Leu Leu Leu Asp Leu Asn Ala
265 225 230 235 240
267 Thr Asp Pro Asp Glu Gly Ala Asn Gly Lys Ile Val Tyr Ser Phe Ser
268 245 250 255
270 Ser His Val Ser Pro Lys Ile Met Glu Thr Phe Lys Ile Asp Ser Glu
271 260 265 270
273 Lys Ser Tyr Glu Ile Asp Val Gln Ala Gln Asp Leu Gly Pro Asn Ser
274 275 280 285
276 Ile Pro Ala His Cys Lys Ile Ile Ile Lys Val Val Asp Val Asn Asp
277 290 295 300
279 Asn Lys Pro Glu Ile Asn Ile Asn Leu Met Ser Pro Gly Lys Glu Glu
280 305 310 315 320
282 Ile Ser Tyr Ile Phe Glu Gly Asp Pro Ile Asp Thr Phe Val Ala Leu
283 325 330 335
285 Val Arg Val Gln Asp Lys Asp Ser Gly Leu Asn Gly Glu Ile Val Cys
286 340 345 350
288 Asn Asn Tyr Leu Ile Leu Thr Asn Ala Thr Leu Asp Arg Glu Lys Arg
289 355 360 365
291 Ser Glu Tyr Ser Leu Thr Val Ile Ala Glu Asp Arg Gly Thr Pro Ser
292 370 375 380
294 Leu Ser Thr Val Lys His Phe Thr Val Gln Ile Asn Asp Ile Asn Asp

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
TIME: 13:45:10

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

295	385	390	395	400	
297	Asn	Pro	Pro	His	
			Phe	Gln	
			Arg	Arg	
			Ser	Ser	
			Arg	Tyr	
			Glu	Phe	
			Val	Val	
			Ile	Ser	
			Glu		
298		405	410	415	
300	Asn	Asn	Ser	Pro	
			Gly	Ala	
			Tyr	Ile	
			Thr	Thr	
			Val	Thr	
			Ala	Thr	
			Asp	Pro	
301		420	425	430	
303	Phe	Ile	Leu	Gly	
			Ser	Ser	
			Ile	Thr	
			Thr	Tyr	
			Val	Thr	
			Ile	Asp	
			Pro	Ser	
304		435	440	445	
306	Asn	Gly	Ala	Ile	
			Tyr	Ala	
			Leu	Arg	
			Ile	Phe	
			Asp	His	
			Glu	Glu	
			Val	Val	
307		450	455	460	
309	Gln	Ile	Thr	Phe	
			Val	Val	
			Glu	Ala	
			Arg	Asp	
			Gly	Gly	
			Ser	Pro	
			Lys	Gln	
310		465	470	475	480
312	Leu	Val	Ser	Asn	
			Thr	Thr	
			Val	Val	
			Ieu	Thr	
			Ile	Asp	
			Glu	Asn	
313		485	490	495	
315	Asn	Val	Pro	Val	
			Val	Ile	
			Gly	Pro	
			Ala	Leu	
			Arg	Asn	
			Asn	Thr	
			Ala	Glu	
316		500	505	510	
318	Ile	Thr	Ile	Pro	
			Lys	Gly	
			Ala	Glu	
			Ser	Gly	
			Phe	His	
			His	Val	
			Thr	Arg	
319		515	520	525	
321	Ala	Ile	Val	Ala	
			Gly	Asn	
			Glu	Asn	
			Ile	Phe	
			Ile	Ile	
			Asp	Pro	
322		530	535	540	
324	Ser	Cys	Asp	Ile	
			His	Thr	
			Asn	Val	
			Ser	Met	
			Asp	Ser	
			Val	Pro	
			Tyr	Thr	
325		545	550	555	560
327	Glu	Tyr	Glu	Leu	
			Ser	Val	
			Ile	Ile	
			Gln	Asp	
			Lys	Gly	
			Asn	Pro	
			Gln	Leu	
328		565	570	575	
330	His	Thr	Lys	Val	
			Leu	Leu	
			Lys	Cys	
			Met	Ile	
			Phe	Glu	
			Tyr	Ala	
			Glu	Ser	
331		580	585	590	
333	Val	Thr	Ser	Thr	
			Ala	Met	
			Thr	Ser	
			Val	Gln	
			Ala	Ser	
			Leu	Asp	
334		595	600	605	
336	Leu	Val	Ile	Met	
			Val	Leu	
			Phe	Ala	
			Thr	Arg	
			Cys	Asn	
			Arg	Glu	
			Lys	Lys	
337		610	615	620	
339	Asp	Thr	Arg	Ser	
			Tyr	Asn	
			Cys	Arg	
			Val	Ala	
			Glu	Ser	
			Thr	Tyr	
340		625	630	635	640
342	His	Pro	Lys	Arg	
			Pro	Ser	
			Arg	Gln	
			Ile	His	
			Lys	Gly	
			Asp	Ile	
			Thr	Leu	
343		645	650	655	
345	Val	Pro	Thr	Ile	
			Asn	Gly	
			Thr	Leu	
			Pro	Ile	
			Arg	Arg	
			Ser	His	
346		660	665	670	
348	Ser	Pro	Ser	Ser	
			Pro	Thr	
			Leu	Glu	
			Arg	Gly	
			Gln	Met	
			Gly	Ser	
349		675	680	685	
351	Ser	Ser	Asn	His	
			Val	Pro	
			Glu	Asn	
			Phe	Ser	
			Leu	Glu	
			Ieu	Ieu	
			Thr	His	
352		690	695	700	
354	Thr	Pro	Ala	Val	
			Glu	Gln	
			Val	Ser	
			Gln	Leu	
			Leu	Ser	
			Met	Leu	
			His	Gln	
355		705	710	715	720
357	Gly	Gln	Tyr	Gln	
			Pro	Arg	
			Pro	Ser	
			Phe	Arg	
			Gly	Asn	
			Lys	Tyr	
			Ser	Arg	
358		725	730	735	
360	Ser	Tyr	Arg	Tyr	
			Ala	Leu	
			Gln	Asp	
			Met	Asp	
			Lys	Phe	
			Ser	Leu	
			Lys	Asp	
361		740	745	750	
363	Ser	Gly	Arg	Gly	
			Asp	Ser	
			Glu	Ala	
			Gly	Asp	
			Ser	Asp	
			Tyr	Asp	
			Leu	Gly	
364		755	760	765	
366	Arg	Asp	Ser	Pro	
			Ile	Asp	
			Arg	Arg	
			Leu	Leu	
			Gly	Gly	
			Phe	Ser	
			Asp	Leu	
367		770	775	780	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
TIME: 13:45:10

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

369 Glu Glu Cys Arg Val Leu Gly His Ser Asp Gln Cys Trp Met Pro Pro
370 785 790 795 800
372 Leu Pro Ser Pro Ser Ser Asp Tyr Arg Ser Asn Met Phe Ile Pro Gly
373 805 810 815
375 Glu Glu Phe Pro Thr Gln Pro Gln Gln His Pro His Gln Ser Leu
376 820 825 830
378 Glu Asp Asp Ala Gln Pro Ala Asp Ser Gly Glu Lys Lys Lys Ser Phe
379 835 840 845
381 Ser Thr Phe Gly Lys Asp Ser Pro Asn Asp Glu Asp Thr Gly Asp Thr
382 850 855 860
384 Val Asp Arg Ser Asn Ser Leu Glu Arg Arg Lys Gly Pro Leu Pro Ala
385 865 870 875 880
387 Glu Glu Ile Pro Glu Asn Tyr Glu Glu Asp Asp Phe Asp Asn Val Leu
388 885 890 895
390 Leu Val Ala Glu Ile Asn Lys Leu Leu Gln Asp Val Arg Gln Ser
E--> 391 900 905 910
407 <210> SEQ ID NO: 5
408 <211> LENGTH: 1124 - 1124 listed
409 <212> TYPE: PRT - 884 shown
410 <213> ORGANISM: Homo sapiens
412 <400> SEQUENCE: 5
413 Lys Asn Leu Lys Tyr Arg Ile Tyr Glu Glu Gln Arg Val Gly Ser Val
414 1 5 10 15
416 Ile Ala Arg Leu Ser Glu Asp Val Ala Asp Val Leu Leu Lys Leu Pro
417 20 25 30
419 Asn Pro Ser Thr Val Arg Phe Arg Ala Met Gln Arg Gly Asn Ser Pro
420 35 40 45
422 Leu Leu Val Val Asn Glu Asp Asn Gly Glu Ile Ser Ile Gly Ala Thr
423 50 55 60
425 Glu Phe Asp Val Ile Thr Leu Pro Thr Glu His Leu Gln Leu Phe His
426 65 70 75 80
428 Ile Glu Val Glu Val Leu Asp Ile Asn Asp Asn Ser Pro Gln Phe Ser
429 85 90 95
431 Arg Ser Leu Ile Pro Ile Glu Ile Ser Glu Ser Ala Ala Val Gly Thr
432 100 105 110
434 Arg Ile Pro Leu Asp Ser Ala Phe Asp Pro Asp Val Gly Glu Asn Ser
435 115 120 125
437 Leu His Thr Tyr Ser Leu Ser Ala Asn Asp Phe Phe Asn Ile Glu Val
438 130 135 140
440 Arg Thr Arg Thr Asp Gly Ala Lys Tyr Ala Glu Leu Ile Val Val Arg
441 145 150 155 160
443 Ala Ser Asp Met Gly Val Pro Gln Arg Ser Gly Ser Ser Ile Leu Lys
444 165 170 175
446 Ile Ser Ile Ser Asp Ser Asn Asp Ser Pro Ala Phe Glu Gln Gln
447 180 185 190
449 Ser Tyr Ile Ile Gln Leu Leu Glu Asn Ser Pro Val Gly Thr Leu Leu
450 195 200 205
452 Leu Asp Leu Asn Ala Thr Asp Pro Asp Glu Gly Ala Asn Gly Lys Ile
453 210 215 220

Set #3
- 911 shown
- 1151 listed

RAW SEQUENCE LISTING DATE: 01/29/2001
 PATENT APPLICATION: US/09/759,130 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

455 Val Tyr Ser Phe Ser Ser His Val Ser Pro Lys Ile Met Glu Thr Phe
 456 225 230 235 240
 458 Asp Tyr Glu Ile Thr Lys Ser Tyr Glu Ile Asp Val Gln Ala Gln Asp
 459 245 250 255
 461 Leu Gly Pro Asn Ser Ile Pro Ala His Cys Lys Ile Ile Ile Lys Val
 462 260 265 270
 464 Val Asp,Val Asn Asp Asn Lys Pro Glu Ile Asn Ile Asn Leu Met Ser
 465 275 280 285
 467 Pro Gly Lys Glu Glu Ile Ser Tyr Ile Phe Glu Gly Asp Pro Ile Asp
 468 290 295 300
 470 Thr Phe Val Ala Leu Val Arg Val Gln Asp Lys Asp Ser Gly Leu Asn
 471 305 310 315 320
 473 Gln Lys Thr Tyr Glu Asn Asn Tyr Leu Ile Leu Thr Asn Ala Thr Leu
 474 325 330 335
 476 Asp Arg Glu Lys Arg Ser Glu Tyr Ser Leu Thr Val Ile Ala Glu Asp
 477 340 345 350
 479 Arg Gly Thr Pro Ser Leu Ser Thr Val Lys His Phe Thr Val Gln Ile
 480 355 360 365
 482 Asn Asp Ile Asn Asp Asn Pro Pro His Phe Gln Arg Ser Arg Tyr Glu
 483 370 375 380
 485 Phe Val Ile Ser Glu Asn Asn Ser Pro Gly Ala Tyr Ile Thr Thr Val
 486 385 390 395 400
 488 Thr Ala Thr Asp Pro Asp Leu Gly Glu Asn Gly Gln Val Thr Tyr Thr
 489 405 410 415
 491 Thr Ile Asp Pro Ser Asn Gly Ala Ile Tyr Ala Leu Arg Ile Phe Asp
 492 420 425 430
 494 His Glu Glu Val Ser Gln Ile Thr Phe Val Val Glu Ala Arg Asp Gly
 495 435 440 445
 497 Gly Ser Pro Lys Gln Leu Val Ser Asn Thr Thr Val Val Leu Thr Ile
 498 450 455 460
 500 Ile Asp Glu Asn Asp Asn Val Pro Val Val Ile Gly Pro Ala Leu Arg
 501 465 470 475 480
 503 Asn Asn Thr Ala Glu Ile Thr Ile Pro Lys Gly Ala Glu Ser Gly Phe
 504 485 490 495
 506 Ala Glu Leu Ser Cys Ala Ile Val Ala Gly Asn Glu Glu Asn Ile Phe
 507 500 505 510
 509 Ile Ile Asp Pro Arg Ser Cys Asp Ile His Thr Asn Val Ser Met Asp
 510 515 520 525
 512 Ser Val Pro Tyr Thr Glu Trp Glu Leu Ser Val Ile Ile Gln Asp Lys
 513 530 535 540
 515 Gly Asn Pro Gln Leu His Thr Lys Val Leu Leu Lys Cys Met Ile Phe
 516 545 550 555 560
 518 Glu Tyr Ala Glu Ser Val Thr Ser Thr Ala Met Thr Ser Val Ser Gln
 519 565 570 575
 521 Ile Cys Ala Val Leu Leu Val Ile Met Val Leu Phe Ala Thr Arg Cys
 522 580 585 590
 524 Asn Arg Glu Lys Lys Asp Thr Arg Ser Tyr Asn Cys Arg Val Ala Glu
 525 595 600 605
 527 Ser Thr Tyr Gln His His Pro Lys Arg Pro Ser Arg Gln Ile His Lys

RAW SEQUENCE LISTING DATE: 01/29/2001
 PATENT APPLICATION: US/09/759,130 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

528 610 615 620
 530 Gly Asp Ile Thr Leu Val Pro Thr Ile Asn Gly Thr Leu Pro Ile Arg
 531 625 630 635 640
 533 Ser His His Arg Ser Ser Pro Ser Ser Ser Pro Thr Leu Glu Arg Gly
 534 645 650 655
 536 Gln Met Gly Ser Arg Gln Ser His Asn Ser His Gln Ser Leu Asn Ser
 537 660 665 670
 539 Glu Leu Thr His Ala Thr Pro Ala Val Glu Gln Val Ser Gln Leu Leu
 540 675 680 685
 542 Ser Met Leu His Gln Gly Gln Tyr Gln Pro Arg Pro Ser Phe Arg Gly
 543 690 695 700
 545 Asn Lys Tyr Ser Arg Ser Tyr Arg Tyr Ala Leu Gln Asp Met Asp Lys
 546 705 710 715 720
 548 Phe Ser Leu Lys Asp Ser Gly Arg Gly Asp Ser Glu Ala Gly Asp Ser
 549 725 730 735
 551 Asp Tyr Asp Leu Gly Arg Asp Ser Pro Ile Asp Arg Leu Leu Gly Glu
 552 740 745 750
 554 Met Arg Leu Cys Thr Glu Glu Cys Arg Val Leu Gly His Ser Asp Gln
 555 755 760 765
 557 Cys Trp Met Pro Pro Leu Pro Ser Pro Ser Ser Asp Tyr Arg Ser Asn
 558 770 775 780
 560 Met Phe Ile Pro Gly Glu Glu Phe Pro Thr Gln Pro Gln Gln His
 561 785 790 795 800
 563 Pro His Gln Ser Leu Glu Asp Asp Ala Gln Pro Ala Asp Ser Gly Glu
 564 805 810 815
 566 Lys Lys Lys Ser Phe Ser Thr Phe Gly Lys Asp Ser Pro Asn Asp Glu
 567 820 825 830
 569 Ser Ser Val Phe Gln Arg Leu Leu Pro Pro Ser Leu Asp Thr Tyr Ser
 570 835 840 845
 572 Gly Pro Pro Leu Gly Thr His Ser Ser Val Gln Pro Ser Ser Lys Trp
 573 850 855 860
 575 Met Asp Ala Ser Glu Leu Val Ala Glu Ile Asn Lys Leu Leu Gln Asp
 576 865 870 875 880
 E--> 578 Val Arg Gln Ser - 884 shown seg #5
 582 <210> SEQ ID NO: 6
 583 <211> LENGTH: 679
 584 <212> TYPE: PRT
 585 <213> ORGANISM: Homo sapiens
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 591 Ile Ala Arg Leu Ser Glu Asp Val Ala Asp Val Leu Leu Lys Leu Pro
 592 20 25 30
 594 Asn Pro Ser Thr Val Arg Phe Arg Ala Met Gln Arg Gly Asn Ser Pro
 595 35 40 45
 597 Leu Leu Val Val Asn Glu Asp Asn Gly Glu Ile Ser Ile Gly Ala Thr
 598 50 55 60
 600 Glu Phe Asp Val Ile Thr Leu Pro Thr Glu His Leu Gln Leu Phe His
 601 65 70 75 80

- 1124 listed

679 listed
 583 found

RAW SEQUENCE LISTING DATE: 01/29/2001
 PATENT APPLICATION: US/09/759,130 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

603 Ile Glu Val Glu Val Leu Asp Ile Asn Asp Asn Ser Pro Gln Phe Ser
 604 85 90 95
 606 Arg Ser Leu Ile Pro Ile Glu Ile Ser Glu Ser Ala Ala Val Gly Thr
 607 100 105 110
 609 Arg Ile Pro Leu Asp Ser Ala Phe Asp Pro Asp Val Gly Glu Asn Ser
 610 115 120 125
 612 Leu His Thr Tyr Ser Leu Ser Ala Asn Asp Phe Phe Asn Ile Glu Val
 613 130 135 140
 615 Arg Thr Arg Thr Asp Gly Ala Lys Tyr Ala Glu Leu Ile Val Val Arg
 616 145 150 155 160
 618 Ala Ser Asp Met Gly Val Pro Gln Arg Ser Gly Ser Ser Ile Leu Lys
 619 165 170 175
 621 Ile Ser Ile Ser Asp Ser Asn Asp Asn Ser Pro Ala Phe Glu Gln Gln
 622 180 185 190
 624 Ser Tyr Ile Ile Gln Leu Leu Glu Asn Ser Pro Val Gly Thr Leu Leu
 625 195 200 205
 627 Leu Asp Leu Asn Ala Thr Asp Pro Asp Glu Gly Ala Asn Gly Lys Ile
 628 210 215 220
 630 Val Tyr Ser Phe Ser Ser His Val Ser Pro Lys Ile Met Glu Thr Phe
 631 225 230 235 240
 633 Asp Tyr Glu Ile Thr Lys Ser Tyr Glu Ile Asp Val Gln Ala Gln Asp
 634 245 250 255
 636 Leu Gly Pro Asn Ser Ile Pro Ala His Cys Lys Ile Ile Ile Lys Val
 637 260 265 270
 639 Val Asp Val Asn Asp Asn Lys Pro Glu Ile Asn Ile Asn Leu Met Ser
 640 275 280 285
 642 Pro Gly Lys Glu Glu Ile Ser Tyr Ile Phe Glu Gly Asp Pro Ile Asp
 643 290 295 300
 645 Thr Phe Val Ala Leu Val Arg Val Gln Asp Lys Asp Ser Gly Leu Asn
 646 305 310 315 320
 648 Gln Lys Thr Tyr Glu Asn Asn Tyr Leu Ile Leu Thr Asn Ala Thr Leu
 649 325 330 335
 651 Asp Arg Glu Lys Arg Ser Glu Tyr Ser Leu Thr Val Ile Ala Glu Asp
 652 340 345 350
 654 Arg Gly Thr Pro Ser Leu Ser Thr Val Lys His Phe Thr Val Gln Ile
 655 355 360 365
 657 Asn Asp Ile Asn Asp Asn Pro Pro His Phe Gln Arg Ser Arg Tyr Glu
 658 370 375 380
 660 Phe Val Ile Ser Glu Asn Asn Ser Pro Gly Ala Tyr Ile Thr Thr Val
 661 385 390 395 400
 663 Thr Ala Thr Asp Pro Asp Leu Gly Glu Asn Gly Gln Val Thr Tyr Thr
 664 405 410 415
 666 Thr Ile Asp Pro Ser Asn Gly Ala Ile Tyr Ala Leu Arg Ile Phe Asp
 667 420 425 430
 669 His Glu Glu Val Ser Gln Ile Thr Phe Val Val Glu Ala Arg Asp Gly
 670 435 440 445
 672 Gly Ser Pro Lys Gln Leu Val Ser Asn Thr Thr Val Val Leu Thr Ile
 673 450 455 460
 675 Ile Asp Glu Asn Asp Asn Val Pro Val Val Ile Gly Pro Ala Leu Arg

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
TIME: 13:45:10

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\1759130.raw

676 465 470 475 480
678 Asn Asn Thr Ala Glu Ile Thr Ile Pro Lys Gly Ala Glu Ser Gly Phe
679 485 490 495
681 Ala Glu Leu Ser Cys Ala Ile Val Ala Gly Asn Glu Glu Asn Ile Phe
682 500 505 510
684 Ile Ile Asp Pro Arg Ser Cys Asp Ile His Thr Asn Val Ser Met Asp
685 515 520 525
687 Ser Val Pro Tyr Thr Glu Trp Glu Leu Ser Val Ile Ile Gln Asp Lys
688 530 535 540
690 Gly Asn Pro Gln Leu His Thr Lys Val Leu Leu Lys Cys Met Ile Phe
691 545 550 555 560
693 Glu Tyr Ala Glu Ser Val Thr Ser Thr Ala Met Thr Ser Val Ser Gln
694 565 570 575
696 Ala Ser Leu Asp Val Ser Met 583 shown seg. #6
E--> 697 580 679 listed
700 <210> SEQ ID NO: 7
701 <211> LENGTH: 22
702 <212> TYPE: PRT
703 <213> ORGANISM: Homo sapiens
705 <400> SEQUENCE: 7
E--> 706 Ile Ile Ile Ile Ser 6 Leu Gly Ala Ile Cys Ala Val Leu Leu Val
E--> 707 1 5 10 15 16 -22 listed
710 <210> SEQ ID NO: 8
711 <211> LENGTH: 423
712 <212> TYPE: PRT
713 <213> ORGANISM: Homo sapiens
715 <400> SEQUENCE: 8
716 Thr Arg Cys Asn Arg Glu Lys Lys Asp Thr Arg Ser Tyr Asn Cys Arg
717 1 5 10 15
719 Val Ala Glu Ser Thr Tyr Gln His His Pro Lys Arg Pro Ser Arg Gln
720 20 25 30
722 Ile His Lys Gly Asp Ile Thr Leu Val Pro Thr Ile Asn Gly Thr Leu
723 35 40 45
725 Pro Ile Arg Ser His His Arg Ser Ser Pro Ser Ser Pro Thr Leu
726 50 55 60
728 Glu Arg Gly Gln Met Gly Ser Arg Gln Ser His Asn Ser His Gln Ser
729 65 70 75 80
731 Phe Ser Leu Glu Leu Thr His Ala Thr Pro Ala Val Glu Gln Val Ser
732 85 90 95
734 Gln Leu Leu Ser Met Leu His Gln Gly Gln Tyr Gln Pro Arg Pro Ser
735 100 105 110
737 Phe Arg Gly Asn Lys Tyr Ser Arg Ser Tyr Arg Tyr Ala Leu Gln Asp
738 115 120 125
740 Met Asp Lys Phe Ser Leu Lys Asp Ser Gly Arg Gly Asp Ser Glu Ala
741 130 135 140
743 Gly Asp Ser Asp Tyr Asp Leu Gly Arg Asp Ser Pro Ile Asp Arg Leu
744 145 150 155 160
746 Pro Ala Ala Met Arg Leu Cys Thr Glu Glu Cys Arg Val Leu Gly His
747 165 170 175

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
TIME: 13:45:10

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\1759130.raw

749 Ser Asp Gln Cys Trp Met Pro Pro Leu Pro Ser Pro Ser Asp Tyr
750 180 185 190
752 Arg Ser Asn Met Phe Ile Pro Gly Glu Glu Phe Pro Thr Glu Pro Gln
753 195 200 205
755 Gln Gln His Pro His Gln Ser Leu Glu Asp Asp Ala Gln Pro Ala Asp
756 210 215 220
758 Ser Gly Glu Lys Lys Ser Phe Ser Thr Phe Gly Lys Asp Ser Pro
759 225 230 235 240
761 Ser Glu Met Ser Ser Val Phe Gln Arg Leu Leu Pro Pro Ser Leu Asp
762 245 250 255
764 Thr Asn Cys Gly Pro Pro Leu Gly Thr His Ser Ser Val Gln Pro Ser
765 260 265 270
767 His Glu Leu Met Asp Ala Ser Glu Leu Val Ala Glu Ile Asn Lys Leu
768 275 280 285
770 Leu Gln Asp Val Arg Gln Ser
E--> 771 290 295 295 shown, 423 listed
1043 <210> SEQ ID NO: 33
1044 <211> LENGTH: 1150
1045 <212> TYPE: PRT
1046 <213> ORGANISM: Homo sapiens
1048 <400> SEQUENCE: 33
1049 Met His Gln Met Asn Ala Lys Met His Phe Arg Phe Val Phe Ala Leu
1050 1 5 10 15
1052 Leu Ile Val Ser Phe Asn His Asp Val Leu Gly Lys Asn Leu Lys Tyr
1053 20 25 30
1055 Arg Ile Tyr Glu Glu Gln Arg Val Gly Ser Val Ile Ala Arg Leu Ser
1056 35 40 45
1058 Glu Asp Val Ala Asp Val Leu Leu Lys Leu Pro Asn Pro Ser Thr Val
1059 50 55 60
1061 Arg Phe Arg Ala Met Gln Arg Gly Asn Ser Pro Leu Leu Val Val Asn
1062 65 70 75 80
1064 Glu Asp Asn Gly Glu Ile Ser Ile Gly Ala Thr Ile Asp Arg Glu Gln
1065 85 90 95
1067 Thr Leu Pro Thr Glu His Leu Gln Leu Phe His Ile Glu Val Gln Val
1068 100 105 110
1070 Leu Asp Ile Asn Asp Asn Ser Pro Gln Phe Ser Arg Ser Leu Ile Pro
1071 115 120 125
1073 Ile Glu Ile Ser Glu Ser Ala Ala Val Gly Thr Arg Ile Pro Leu Asp
1074 130 135 140
1076 Ser Ala Phe Asp Pro Asp Val Gly Glu Asn Ser Leu His Thr Tyr Ser
1077 145 150 155 160
1079 Leu Ser Ala Asn Asp Phe Phe Asn Ile Glu Val Arg Thr Arg Thr Asp
1080 165 170 175
1082 Glu Leu Lys Ser Ser Tyr Glu Leu Gln Leu Thr Ala Ser Asp Met Gly
1083 180 185 190
1085 Val Pro Gln Arg Ser Gly Ser Ser Ile Leu Lys Ile Ser Ile Ser Asp
1086 195 200 205
1088 Ser Asn Asp Asn Ser Pro Ala Phe Glu Gln Gln Ser Tyr Ile Ile Gln
1089 210 215 220

295 shown, 423 listed

1150 listed, 910 shown

RAW SEQUENCE LISTING DATE: 01/29/2001
 PATENT APPLICATION: US/09/759,130 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

1091 Leu Leu Glu Asn Ser Pro Val Gly Thr Leu Leu Asp Leu Asn Ala
 1092 225 230 235 240
 1094 Thr Asp Pro Asp Glu Gly Ala Asn Gly Lys Ile Val Tyr Ser Phe Ser
 1095 245 250 255
 1097 Ser His Val Ser Pro Lys Ile Met Glu Thr Phe Lys Ile Asp Ser Glu
 1098 260 265 270
 1100 Lys Ser Tyr Glu Ile Asp Val Gln Ala Gln Asp Leu Gly Pro Asn Ser
 1101 275 280 285
 1103 Ile Pro Ala His Cys Lys Ile Ile Ile Lys Val Val Asp Val Asn Asp
 1104 290 295 300
 1106 Asn Lys Pro Glu Ile Asn Ile Asn Leu Met Ser Pro Gly Lys Glu Glu
 1107 305 310 315 320
 1109 Ile Ser Tyr Ile Phe Glu Gly Asp Pro Ile Asp Thr Phe Val Ala Leu
 1110 325 330 335
 1112 Val Arg Val Gln Asp Lys Asp Ser Gly Leu Asn Gly Glu Ile Val Cys
 1113 340 345 350
 1115 Asn Asn Tyr Leu Ile Leu Thr Asn Ala Thr Leu Asp Arg Glu Lys Arg
 1116 355 360 365
 1118 Ser Glu Tyr Ser Leu Thr Val Ile Ala Glu Asp Arg Gly Thr Pro Ser
 1119 370 375 380
 1121 Leu Ser Thr Val Lys His Phe Thr Val Gln Ile Asn Asp Ile Asn Asp
 1122 385 390 395 400
 1124 Asn Pro Pro His Phe Gln Arg Ser Arg Tyr Glu Phe Val Ile Ser Glu
 1125 405 410 415
 1127 Asn Asn Ser Pro Gly Ala Tyr Ile Thr Thr Val Thr Ala Thr Asp Pro
 1128 420 425 430
 1130 Phe Ile Leu Gly Ser Ser Ile Thr Thr Tyr Val Thr Ile Asp Pro Ser
 1131 435 440 445
 1133 Asn Gly Ala Ile Tyr Ala Leu Arg Ile Phe Asp His Glu Glu Val Ser
 1134 450 455 460
 1136 Gln Ile Thr Phe Val Val Glu Ala Arg Asp Gly Gly Ser Pro Lys Gln
 1137 465 470 475 480
 1139 Leu Val Ser Asn Thr Thr Val Val Leu Thr Ile Ile Asp Glu Asn Asp
 1140 485 490 495
 1142 Asn Val Pro Val Val Ile Gly Pro Ala Leu Arg Asn Asn Thr Ala Glu
 1143 500 505 510
 1145 Ile Thr Ile Pro Lys Gly Ala Glu Ser Gly Phe His Val Thr Arg Ile
 1146 515 520 525
 1148 Ala Ile Val Ala Gly Asn Glu Asn Ile Phe Ile Ile Asp Pro Arg
 1149 530 535 540
 1151 Ser Cys Asp Ile His Thr Asn Val Ser Met Asp Ser Val Pro Tyr Thr
 1152 545 550 555 560
 1154 Glu Trp Glu Leu Ser Val Ile Ile Gln Asp Lys Gly Asn Pro Gln Leu
 1155 565 570 575
 1157 His Thr Lys Val Leu Leu Lys Cys Met Ile Phe Glu Tyr Ala Glu Ser
 1158 580 585 590
 1160 Val Thr Ser Thr Ala Met Thr Ser Val Ser Gln Ala Ser Leu Asp Val
 1161 595 600 605
 1163 Leu Val Ile Met Val Leu Phe Ala Thr Arg Cys Asn Arg Glu Lys Lys

RAW SEQUENCE LISTING DATE: 01/29/2001
 PATENT APPLICATION: US/09/759,130 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\1759130.raw

1164 610 615 620
 1166 Asp Thr Arg Ser Tyr Asn Cys Arg Val Ala Glu Ser Thr Tyr Gln His
 1167 625 630 635 640
 1169 His Pro Lys Arg Pro Ser Arg Gln Ile His Lys Gly Asp Ile Thr Leu
 1170 645 650 655
 1172 Val Pro Thr Ile Asn Gly Thr Leu Pro Ile Arg Ser His His Arg Ser
 1173 660 665 670
 1175 Ser Pro Ser Ser Pro Thr Leu Glu Arg Gly Gln Met Gly Ser Arg
 1176 675 680 685
 1178 Ser Ser Asn His Val Pro Glu Asn Phe Ser Leu Glu Leu Thr His Ala
 1179 690 695 700
 1181 Thr Pro Ala Val Glu Val Ser Gln Leu Leu Ser Met Leu His Gln Gly
 1182 705 710 715 720
 1184 Gln Tyr Gln Pro Arg Pro Ser Phe Arg Gly Asn Lys Tyr Ser Arg Ser
 1185 725 730 735
 1187 Tyr Arg Tyr Ala Leu Gln Asp Met Asp Lys Phe Ser Leu Lys Asp Ser
 1188 740 745 750
 1190 Gly Arg Gly Asp Ser Glu Ala Gly Asp Ser Asp Tyr Asp Leu Gly Arg
 1191 755 760 765
 1193 Asp Ser Pro Ile Asp Arg Leu Leu Gly Glu Gly Phe Ser Asp Leu Phe
 1194 770 775 780
 1196 Glu Cys Arg Val Leu Gly His Ser Asp Gln Cys Trp Met Pro Pro Leu
 1197 785 790 795 800
 1199 Pro Ser Pro Ser Ser Tyr Arg Ser Asn Met Phe Ile Pro Gly Glu
 1200 805 810 815
 1202 Glu Phe Pro Thr Gln Pro Gln Gln His Pro His Gln Ser Leu Glu
 1203 820 825 830
 1205 Asp Asp Ala Gln Pro Ala Asp Ser Gly Glu Lys Lys Ser Phe Ser
 1206 835 840 845
 1208 Thr Phe Gly Lys Asp Ser Pro Asn Asp Glu Asp Thr Gly Asp Thr Ser
 1209 850 855 860
 1211 Asp Arg Ser Asn Ser Ile Glu Arg Arg Lys Gly Pro Leu Pro Ala Lys
 1212 865 870 875 880
 1214 Asn His Leu Asn Asp Gly Lys His Glu Leu Met Asp Ala Ser Glu Leu
 1215 885 890 895
 1217 Val Ala Glu Ile Asn Lys Leu Leu Gln Asp Val Arg Gln Ser
 E--> 1218 900 905 910 1150 listed seg # 33
 1226 <210> SEQ ID NO: 35
 1227 <211> LENGTH: 1123 1123 listed, 883 shown
 1228 <212> TYPE: PRT
 1229 <213> ORGANISM: Homo sapiens
 1231 <400> SEQUENCE: 35
 1232 Lys Asn Leu Lys Tyr Arg Ile Tyr Glu Glu Gln Arg Val Gly Ser Val
 1233 1 5 10 15
 1235 Ile Ala Arg Leu Ser Glu Asp Val Ala Asp Val Leu Leu Lys Leu Pro
 1236 20 25 30
 1238 Asn Pro Ser Thr Val Arg Phe Arg Ala Met Gln Arg Gly Asn Ser Pro
 1239 35 40 45
 1241 Leu Leu Val Val Asn Glu Asp Asn Gly Glu Ile Ser Ile Gly Ala Thr

1150 listed
 910 shown

RAW SEQUENCE LISTING DATE: 01/29/2001
 PATENT APPLICATION: US/09/759,130 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\1759130.raw

1242	50	55	60														
1244	Glu	Phe	Asp	Val	Ile	Thr	Leu	Pro	Thr	Glu	His	Leu	Gln	Leu	Phe	His	
1245	65											75				80	
1247	Ile	Glu	Val	Glu	Val	Leu	Asp	Ile	Asn	Asp	Asn	Ser	Pro	Gln	Phe	Ser	
1248												85				95	
1250	Arg	Ser	Leu	Ile	Pro	Ile	Glu	Ile	Ser	Glu	Ser	Ala	Ala	Val	Gly	Thr	
1251												100				110	
1253	Arg	Ile	Pro	Leu	Asp	Ser	Ala	Phe	Asp	Pro	Asp	Val	Gly	Glu	Asn	Ser	
1254												115				125	
1256	Leu	His	Thr	Tyr	Ser	Leu	Ser	Ala	Asn	Asp	Phe	Phe	Asn	Ile	Glu	Val	
1257												130				140	
1259	Arg	Thr	Arg	Thr	Asp	Gly	Ala	Lys	Tyr	Ala	Glu	Leu	Ile	Val	Val	Arg	
1260	145											150				160	
1262	Ala	Ser	Asp	Met	Gly	Val	Pro	Gln	Arg	Ser	Gly	Ser	Ser	Ile	Leu	Lys	
1263												165				175	
1265	Ile	Ser	Ile	Ser	Asp	Ser	Asn	Asp	Asn	Ser	Pro	Ala	Phe	Glu	Gln	Gln	
1266												180				190	
1268	Ser	Tyr	Ile	Ile	Gln	Leu	Leu	Glu	Asn	Ser	Pro	Val	Gly	Thr	Leu	Leu	
1269												195				205	
1271	Leu	Asp	Leu	Asn	Ala	Thr	Asp	Pro	Asp	Glu	Gly	Ala	Asn	Gly	Lys	Ile	
1272												210				220	
1274	Val	Tyr	Ser	Phe	Ser	Ser	His	Val	Ser	Pro	Lys	Ile	Met	Glu	Thr	Phe	
1275	225											230				235	
1277	Asp	Tyr	Glu	Ile	Thr	Lys	Ser	Tyr	Glu	Ile	Asp	Val	Gln	Ala	Gln	Asp	
1278												245				255	
1280	Leu	Gly	Pro	Asn	Ser	Ile	Pro	Ala	His	Cys	Lys	Ile	Ile	Ile	Lys	Val	
1281												260				270	
1283	Val	Asp	Val	Asn	Asn	Asp	Asn	Lys	Pro	Glu	Ile	Asn	Ile	Asn	Leu	Met	Ser
1284												275				285	
1286	Pro	Gly	Lys	Glu	Glu	Ile	Ser	Tyr	Ile	Phe	Glu	Gly	Asp	Pro	Ile	Asp	
1287												290				300	
1289	Thr	Phe	Val	Ala	Leu	Val	Arg	Val	Gln	Asp	Lys	Asp	Ser	Gly	Leu	Asn	
1290	305											310				320	
1292	Gln	Lys	Thr	Tyr	Glu	Asn	Asn	Tyr	Leu	Ile	Leu	Thr	Asn	Ala	Thr	Leu	
1293												325				335	
1295	Asp	Arg	Glu	Lys	Arg	Ser	Glu	Tyr	Ser	Leu	Thr	Val	Ile	Ala	Glu	Asp	
1296												340				350	
1298	Arg	Gly	Thr	Pro	Ser	Leu	Ser	Thr	Val	Lys	His	Phe	Thr	Val	Gln	Ile	
1299												355				365	
1301	Asn	Asp	Ile	Asn	Asp	Asn	Pro	Pro	His	Phe	Gln	Arg	Ser	Arg	Tyr	Glu	
1302												370				380	
1304	Phe	Val	Ile	Ser	Glu	Asn	Asn	Ser	Pro	Gly	Ala	Tyr	Ile	Thr	Thr	Val	
1305	385											390				400	
1307	Thr	Ala	Thr	Asp	Pro	Asp	Leu	Gly	Glu	Asn	Gly	Gln	Val	Thr	Tyr	Thr	
1308												405				415	
1310	Thr	Ile	Asp	Pro	Ser	Asn	Gly	Ala	Ile	Tyr	Ala	Leu	Arg	Ile	Phe	Asp	
1311												420				430	
1313	His	Glu	Glu	Val	Ser	Gln	Ile	Thr	Phe	Val	Val	Glu	Ala	Arg	Asp	Gly	
1314												435				445	

RAW SEQUENCE LISTING DATE: 01/29/2001
 PATENT APPLICATION: US/09/759,130 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

1316 Gly Ser Pro Lys Gln Leu Val Ser Asn Thr Thr Val Val Leu Thr Ile
 1317 450 455 460
 1319 Ile Asp Glu Asn Asp Asn Val Pro Val Val Ile Gly Pro Ala Leu Arg
 1320 465 470 475 480
 1322 Asn Asn Thr Ala Glu Ile Thr Ile Pro Lys Gly Ala Glu Ser Gly Phe
 1323 485 490 495
 1325 Ala Glu Leu Ser Cys Ala Ile Val Ala Gly Asn Glu Glu Asn Ile Phe
 1326 500 505 510
 1328 Ile Ile Asp Pro Arg Ser Cys Asp Ile His Thr Asn Val Ser Met Asp
 1329 515 520 525
 1331 Ser Val Pro Tyr Thr Glu Trp Glu Leu Ser Val Ile Ile Gln Asp Lys
 1332 530 535 540
 1334 Gly Asn Pro Gln Leu His Thr Lys Val Leu Leu Lys Cys Met Ile Phe
 1335 545 550 555 560
 1337 Glu Tyr Ala Glu Ser Val Thr Ser Thr Ala Met Thr Ser Val Ser Gln
 1338 565 570 575
 1340 Ile Cys Ala Val Leu Leu Val Ile Met Val Leu Phe Ala Thr Arg Cys
 1341 580 585 590
 1343 Asn Arg Glu Lys Lys Asp Thr Arg Ser Tyr Asn Cys Arg Val Ala Glu
 1344 595 600 605
 1346 Ser Thr Tyr Gln His His Pro Lys Arg Pro Ser Arg Gln Ile His Lys
 1347 610 615 620
 1349 Gly Asp Ile Thr Leu Val Pro Thr Ile Asn Gly Thr Leu Pro Ile Arg
 1350 625 630 635 640
 1352 Ser His His Arg Ser Ser Pro Ser Ser Pro Thr Leu Glu Arg Gly
 1353 645 650 655
 1355 Gln Met Gly Ser Arg Gln Ser His Asn Ser His Gln Ser Leu Asn Ser
 1356 660 665 670
 1358 Glu Leu Thr His Ala Thr Pro Ala Val Glu Val Ser Gln Leu Leu Ser
 1359 675 680 685
 1361 Met Leu His Gln Gly Gln Tyr Gln Pro Arg Pro Ser Phe Arg Gly Asn
 1362 690 695 700
 1364 Lys Tyr Ser Arg Ser Tyr Arg Tyr Ala Leu Gln Asp Met Asp Lys Phe
 1365 705 710 715 720
 1367 Ser Leu Lys Asp Ser Gly Arg Gly Asp Ser Glu Ala Gly Asp Ser Asp
 1368 725 730 735
 1370 Tyr Asp Leu Gly Arg Asp Ser Pro Ile Asp Arg Leu Leu Gly Glu Gly
 1371 740 745 750
 1373 Arg Leu Cys Thr Glu Glu Cys Arg Val Leu Gly His Ser Asp Gln Cys
 1374 755 760 765
 1376 Trp Met Pro Pro Leu Pro Ser Pro Ser Asp Tyr Arg Ser Asn Met
 1377 770 775 780
 1379 Phe Ile Pro Gly Glu Glu Phe Pro Thr Gln Pro Gln Gln His Pro
 1380 785 790 795 800
 1382 His Gln Ser Leu Glu Asp Asp Ala Gln Pro Ala Asp Ser Gly Glu Lys
 1383 805 810 815
 1385 Lys Lys Ser Phe Ser Thr Phe Gly Lys Asp Ser Pro Asn Asp Glu Asp
 1386 820 825 830
 1388 Ser Val Phe Gln Arg Leu Leu Pro Pro Ser Leu Asp Thr Tyr Ser Glu

RAW SEQUENCE LISTING DATE: 01/29/2001
 PATENT APPLICATION: US/09/759,130 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

1389 835 840 845
 1391 Leu Pro Ala Met Glu Glu Ile Pro Glu Asn Tyr Glu Glu Asp Asp Phe
 1392 850 855 860
 1394 Asp Ala Ser Glu Leu Val Ala Glu Ile Asn Lys Leu Leu Gln Asp Val
 1395 865 870 875 880
 E--> 1397 Arg Gln Ser 883
 1411 <210> SEQ ID NO: 38
 1412 <211> LENGTH 423
 1413 <212> TYPE: PRT
 1414 <213> ORGANISM: Homo sapiens
 1416 <400> SEQUENCE: 38
 1417 Ala Thr Arg Cys Asn Arg Glu Lys Lys Asp Thr Arg Ser Tyr Asn Cys
 1418 1 5 10 15
 1420 Arg Val Ala Glu Ser Thr Tyr Gln His His Pro Lys Arg Pro Ser Arg
 1421 20 25 30
 1423 Gln Ile His Lys Gly Asp Ile Thr Leu Val Pro Thr Ile Asn Gly Thr
 1424 35 40 45
 1426 Leu Pro Ile Arg Ser His His Arg Ser Ser Pro Ser Ser Pro Thr
 1427 50 55 60
 1429 Leu Glu Arg Gly Gln Met Gly Ser Arg Glu Ser His Asn Ser His Gln
 1430 65 70 75 80
 1432 Asn Phe Ser Leu Glu Leu Thr His Ala Thr Pro Ala Val Glu Val Ser
 1433 85 90 95
 1435 Gln Leu Leu Ser Met Leu His Gln Gly Gln Tyr Gln Pro Arg Pro Ser
 1436 100 105 110
 1438 Phe Arg Gly Asn Lys Tyr Ser Arg Ser Tyr Arg Tyr Ala Leu Gln Asp
 1439 115 120 125
 1441 Met Asp Lys Phe Ser Leu Lys Asp Ser Gly Arg Gly Asp Ser Glu Ala
 1442 130 135 140
 1444 Gly Asp Ser Asp Tyr Asp Leu Gly Arg Asp Ser Pro Ile Asp Arg Leu
 1445 145 150 155 160
 1447 Pro Ala Ala Met Arg Leu Cys Thr Glu Glu Cys Arg Val Leu Gly His
 1448 165 170 175
 1450 Ser Asp Gln Cys Trp Met Pro Pro Leu Pro Ser Pro Ser Asp Tyr
 1451 180 185 190
 1453 Arg Ser Asn Met Phe Ile Pro Gly Glu Glu Phe Pro Thr Gln Pro Gln
 1454 195 200 205
 1456 Gln Gln His Pro His Gln Ser Leu Glu Asp Asp Ala Gln Pro Ala Asp
 1457 210 215 220
 1459 Ser Gly Glu Lys Lys Ser Phe Ser Thr Phe Gly Lys Asp Ser Pro
 1460 225 230 235 240
 1462 Ser Glu Met Ser Ser Val Phe Gln Arg Leu Leu Pro Pro Ser Leu Asp
 1463 245 250 255
 1465 Thr Asn Cys Gly Pro Pro Leu Gly Thr His Ser Ser Val Gln Pro Ser
 1466 260 265 270
 1468 His Glu Leu Met Asp Ala Ser Glu Leu Val Ala Glu Ile Asn Lys Leu
 1469 275 280 285
 1471 Leu Gln Asp Val Arg Gln Ser
 E--> 1472 290 295
 295

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/759,130

DATE: 01/29/2001
TIME: 13:45:10

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

1594 <210> SEQ ID NO: 42
 1595 <211> LENGTH 1183 1183 listed, 1135 shown
 1596 <212> TYPE: PRT
 1597 <213> ORGANISM: Mus sp.
 1599 <400> SEQUENCE: 42
 1600 Met Met Leu Leu Pro Phe Leu Leu Gly Leu Leu Gly Pro Gly Ser
 1601 1 5 10 15
 1603 Tyr Leu Phe Ile Ser Gly Asp Cys Gln Glu Val Ala Thr Val Met Val
 1604 20 25 30
 1606 Lys Phe Gln Val Thr Glu Glu Val Pro Ser Gly Thr Val Ile Gly Lys
 1607 35 40 45
 1609 Asp Ala Phe Gln Ile Leu Gln Leu Pro Gln Ala Leu Pro Val Gln Met
 1610 50 55 60
 1612 Asn Ser Glu Asp Gly Leu Leu Ser Thr Ser Ser Arg Leu Asp Arg Glu
 1613 65 70 75 80
 1615 Lys Leu Cys Arg Gln Glu Asp Pro Cys Leu Val Ser Phe Asp Val Leu
 1616 85 90 95
 1618 Ala Thr Gly Ala Ser Ala Leu Ile His Val Glu Ile Gln Val Leu Asp
 1619 100 105 110
 1621 Ile Asn Asp His Gln Pro Gln Phe Pro Lys Asp Glu Gln Glu Leu Glu
 1622 115 120 125
 1624 Ile Ser Glu Ser Ala Ser Leu His Thr Arg Ile Pro Leu Asp Arg Ala
 1625 130 135 140
 1627 Leu Asp Gln Asp Thr Gly Pro Asn Ser Leu Tyr Ser Tyr Ser Leu Ser
 1628 145 150 155 160
 1630 Pro Ser Glu His Phe Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr
 1631 165 170 175
 1633 Lys His Ala Glu Leu Val Val Val Lys Glu Leu Asp Arg Glu Leu His
 1634 180 185 190
 1636 Ser Tyr Phe Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro
 1637 195 200 205
 1639 Lys Ser Gly Ile Ser Val Val Lys Val Asn Val Leu Asp Ser Asn Asp
 1640 210 215 220
 1642 Asn Ser Pro Val Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Pro Glu
 1643 225 230 235 240
 1645 Asp Thr Val Pro Gly Thr Leu Leu Ile Asn Leu Thr Ala Thr Asp Pro
 1646 245 250 255
 1648 Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Gly Lys His Val
 1649 260 265 270
 1651 Ser Pro Glu Val Met Asn Thr Phe Gly Ile Asp Ala Lys Thr Gly Gln
 1652 275 280 285
 1654 Ile Ile Leu Arg Gln Ala Leu Asp Tyr Glu Lys Asn Pro Ala Tyr Glu
 1655 290 295 300
 1657 Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn Ser Ile Pro Gly His
 1658 305 310 315 320
 1660 Cys Lys Val Leu Ile Lys Val Leu Asp Val Asn Asp Asn Ala Pro Ser
 1661 325 330 335
 1663 Ile Leu Ile Thr Trp Ala Ser Gln Thr Ser Leu Val Ser Glu Asp Leu
 1664 340 345 350

RAW SEQUENCE LISTING DATE: 01/29/2001
 PATENT APPLICATION: US/09/759,130 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\I759130.raw

1666 Pro Arg Asp Ser Phe Ile Ala Leu Val Ser Ala Asn Asp Leu Asp Ser
 1667 355 360 365
 1669 Gly Asn Asn Gly Leu Val His Cys Trp Leu Asn Gln Glu Leu Gly His
 1670 370 375 380
 1672 Phe Arg Leu Lys Arg Thr Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn
 1673 385 390 395 400
 1675 Ala Thr Leu Asp Arg Glu Gln Trp Pro Ile Tyr Thr Leu Thr Val Phe
 1676 405 410 415
 1678 Ala Gln Asp Gln Gly Pro Gln Pro Leu Ser Ala Glu Lys Glu Leu Gln
 1679 420 425 430
 1681 Ile Gln Val Ser Asp Val Asn Asp Asn Ala Pro Val Phe Glu Lys Ser
 1682 435 440 445
 1684 Arg Tyr Glu Val Ser Thr Trp Glu Asn Asn Pro Pro Ser Leu His Leu
 1685 450 455 460
 1687 Ile Thr Leu Lys Ala His Asp Ala Asp Leu Gly Ser Asn Gly Lys Val
 1688 465 470 475 480
 1690 Ser Tyr Arg Ile Lys Asp Ser Pro Val Ser His Leu Val Ile Ile Asp
 1691 485 490 495
 1693 Phe Glu Thr Gly Glu Val Thr Ala Gln Arg Ser Leu Asp Tyr Glu Gln
 1694 500 505 510
 1696 Met Ala Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Arg Gly Gln Pro
 1697 515 520 525
 1699 Gln Leu Ala Ser Ser Ile Ser Val Trp Val Ser Leu Leu Asp Ala Asn
 1700 530 535 540
 1702 Asp Asn Ala Pro Glu Val Ile Gln Pro Val Leu Ser Glu Gly Lys Ala
 1703 545 550 555 560
 1705 Thr Leu Ser Val Leu Val Asn Ala Ser Thr Gly His Leu Leu Leu Pro
 1706 565 570 575
 1708 Ile Glu Asn Pro Ser Gly Met Asp Pro Ala Gly Thr Gly Ile Pro Pro
 1709 580 585 590
 1711 Lys Ala Thr His Ser Pro Trp Ser Phe Leu Leu Leu Thr Ile Val Ala
 1712 595 600 605
 1714 Arg Asp Ala Asp Ser Gly Ala Asn Gly Glu Leu Phe Tyr Ser Ile Gln
 1715 610 615 620
 1717 Ser Gly Asn Asp Ala His Leu Phe Phe Leu Ser Pro Ser Leu Gly Gln
 1718 625 630 635 640
 1720 Leu Phe Ile Asn Val Thr Asn Ala Ser Ser Leu Ile Gly Ser Gln Trp
 1721 645 650 655
 1723 Asp Leu Gly Ile Val Val Glu Asp Gln Gly Ser Pro Ser Leu Gln Thr
 1724 660 665 670
 1726 Gln Val Ser Leu Lys Val Val Phe Val Thr Ser Val Asp His Leu Arg
 1727 675 680 685
 1729 Asp Ser Ala His Glu Pro Gly Val Leu Ser Thr Pro Ala Leu Ala Leu
 1730 690 695 700
 1732 Ile Cys Leu Ala Val Leu Leu Ala Ile Phe Gly Leu Leu Leu Ala Leu
 1733 705 710 715 720
 1735 Phe Val Ser Ile Cys Arg Thr Glu Arg Lys Asp Asn Arg Ala Tyr Asn
 1736 725 730 735
 1738 Cys Arg Glu Ala Glu Ser Ser Tyr Arg His Gln Pro Lys Arg Pro Gln

RAW SEQUENCE LISTING DATE: 01/29/2001
 PATENT APPLICATION: US/09/759,130 TIME: 13:45:10

Input Set : A:\10147-61.txt
 Output Set: N:\CRF3\01292001\1759130.raw

1739	740	745	750
1741	Lys His Ile Gln Lys Ala Asp Ile His Leu Val Pro Val Leu Arg Ala		
1742	755	760	765
1744	His Glu Asn Glu Thr Asp Glu Val Arg Pro Ser His Lys Asp Thr Ser		
1745	770	775	780
1747	Lys Glu Thr Leu Met Glu Ala Gly Trp Asp Ser Cys Leu Glu Ala Pro		
1748	785	790	795
1750	Phe His Leu Thr Pro Thr Leu Tyr Arg Thr Leu Arg Asn Gln Gly Asn		
1751	805	810	815
1753	Gln Gly Glu Leu Ala Glu Ser Gln Glu Val Leu Gln Asp Thr Phe Asn		
1754	820	825	830
1756	Phe Leu Phe Asn His Pro Arg Gln Arg Asn Ala Ser Arg Glu Asn Leu		
1757	835	840	845
1759	Asn Leu Pro Glu Ser Pro Pro Ala Val Arg Gln Pro Leu Leu Arg Pro		
1760	850	855	860
1762	Leu Lys Val Pro Gly Ser Pro Ile Ala Arg Ala Thr Gly Asp Gln Asp		
1763	865	870	875
1765	Lys Glu Glu Ala Pro Gln Ser Pro Pro Ala Ser Ser Ala Thr Leu Arg		
1766	885	890	895
1768	Arg Gln Arg Asn Phe Asn Gly Lys Val Ser Pro Arg Gly Glu Ser Gly		
1769	900	905	910
1771	Pro His Gln Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe		
1772	915	920	925
1774	Ala Glu Arg Asn Pro Val Glu Glu Pro Ala Gly Asp Ser Pro Pro Val		
1775	930	935	940
1777	Gln Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln		
1778	945	950	955
1780	Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly Gly		
1781	965	970	975
1783	Ser Ser Arg Gly Thr Ile Pro Asp Thr Glu Gly Leu Val Gly Leu Lys		
1784	980	985	990
1786	Pro Ser Gly Gln Ala Glu Pro Asp Leu Glu Glu Gly Pro Pro Ser Pro		
1787	995	1000	1005
1789	Leu Ser Ser Leu Leu Asp Pro Asn Thr Gly Leu Ala Leu Asp Lys Leu		
1790	1010	1015	1020
1792	Ser Pro Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu Thr		
1793	1025	1030	1035
1795	Ser Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Thr Val Gly Pro		
1796	1045	1050	1055
1798	Gly Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
1799	1060	1065	1070
1801	Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Gly Gln His Thr Val		
1802	1075	1080	1085
1804	Pro Val Glu Ala Ala Ser Ala Ala Leu Arg Arg Leu Ser Val Cys Gly		
1805	1090	1095	1100
1807	Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Gly Ala Ser Ala Ser Glu		
1808	1105	1110	1115
1810	Ala Gln Gly Arg Lys Lys Ala Ala Glu Ser Arg Leu Gly Cys Gly		
E--> 1811	1125	1130	1135

seg #42

1135 shown

RAW SEQUENCE LISTING DATE: 01/29/2001
PATENT APPLICATION: US/09/759,130 TIME: 13:45:12

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

9092 <210> SEQ ID NO: 300
9093 <211> LENGTH: 24
9094 <212> TYPE: PRT
9095 <213> ORGANISM: Homo sapiens
9097 <400> SEQUENCE: 300
E--> 9098 Gln Met Val Leu Glu Glu Lys Phe Val Tyr Lys His Asn Val His
E--> 9099 X1 P2 A3 G4 S5 T6 Y7 X8 Y9 X10 Y11 X12 P13 S14 Y15 T16

24 listed, 15 shown
Delete all but the amino acid numbering.

<210> 81 Seg. # 81

<211> 4074

<212> DNA

<213> Homo sapiens

<400> 81

gtggtcgcgg ccgaggtag actgtgaaga aggaagaacg ttgcttggc aaaagagca 60
 tatttcagg agacggggcc cctgcctgcc acaccaagca tttaggcacc aggaagaccc 120
 ccatctgcaa gcaagccatg ccttccaggg agaaagaggc ccctgcagct ccttcattcat 180
 gaactggcac atgatcatct ctgggcttat tggtagtgc cttaaagttt ttgaaatgac 240
 cttatttcta ctttatttcc cacagatttt taacaaaagt aacgatggtt tcaccaccac 300
 caggagctat ggaacagtct cacagatttt tggagcagt tccccaagtc ccaacggctt 360
 cattaccaca aggagctatg gaacagtctg ccccaagac tggaaatttt atcaagcaag 420
 atgttttttc ttatccacat ctgaatcatc ttgaaatgaa agcagggact tttgcaaagg 480
 aaaaggatcc acattggcaa ttgtcaacac gccagagaaa ctgaagttt ttcaggacat 540
 aactgatgtt gagaagtatt ttattggctt aatttacat cgtgaagaga aaagggtggcg 600
 ttggatcaac aactctgtgt tcaatggcaa tggatccat cagaatcaga atttcaactg 660
 tgcaccatt ggcctaacaa agacatttga tgctgcatca tggatcatca gctaccgcag 720
 gatctgttag aagaatgcca aatgatcaca gttccctgtg acaagaacta tacttgcac 780
 tcttttggaa tccatacagg tcgtctggcc aatgattctt ttacttacat atctgtctac 840
 cagtagcggt ccttgcctt ttggaaact gagcttctt cttctgcact gggggactgg 900
 atgctagcca tctccaggag acaggatcag tttacggaa acaactcagt tagtataagag 960
 atgaggtccg cttctgttagt actgagcatt tctgactgat caaaaggcc tagtctgtt 1020
 acagggtttt ttttatttta gcctcagagt ataccatact actagggagt aactgttagag 1080
 tgagaaatttta taaacattat ttagggatta ccatgggta agagggataa acataggtcc 1140
 tgtgacttcg tctctgttct caagggaaacc ccattcacat gcccctccta actccacaag 1200
 cgagggttagc agaggctctc ctcagtcgtga actaagctt ggcttgggg agggctccta 1260
 gtgctgagct tggagcagca cggacagcag cattgtttat ggaatggag agaggtctgg 1320
 gcaggatagg aaccttctt gggccctt tgaagaaaac caggcagccca agggagccaa 1380
 acacactaga tttctgttct tcagcaaagc cctgaagaga cacttaagct aaaaattccc 1440
 ttgtcatatt tctgaaactc cattataaca tatgtaaactc cttgttaacc aaaatttagg 1500
 taagcaggct tccttgctc tgaaggttt ggttactgg ctgtatgg tggatatttt 1560
 taaaattttt gatagtctct tagcaacaa taatcacaat atattcatcc cttcagttct 1620
 ggagaaaagcc tgataccagg cacgcctac tgaccccaag ggcctggca ctgatggca 1680
 tcacattgtat ctagaactgg tccagccgccc gaagagtagg aaaagagaag ggctgctcag 1740
 ggaacattt gctggggca cggaaataagc acatagtaaa aagggacat cagggtaaaa 1800
 tggaaatcac ctgagacagg aaacagggag ttcatttggc cacactggaa gaaaggcaag 1860
 aaagaggaag acaagtctt ggttccctg gctgttctcc acactcaca gacatcagct 1920
 atactctgtt tggtcataa gaaagagaaa agagatgcct ttgtgtttt gagtaagaat 1980
 aattaaacca taaggaagac catgtataaa actgtatggaa ataatagtca ccaaagtaca 2040
 gcacatacca ttttgcgtct aataacaatg tagcacagta atgactgtac atgtcattgt 2100
 atgtatacca aacaagattt ttgtaaatca tatttttat tacaacacta agttctgctt 2160
 ctgcattcct aggtttcatc atttttggct ctttagcatg gccacttaca attttttaac 2220
 atgagataac acatcagggt tcagaacttg cttgaaggaa attaccagaa gtaatttgc 2280
 tttgagatgg ggtggaaatt ggaatttatat tagtagccgg tggagataca agttctctga 2340
 ctgtgttggg aaaggataag tgctaccgtt gagaaggaa gaaaggctga gtctaggtgg 2400
 agaaaaatataa caacagaact ctggccaaag gcaagccca gaactcagac aacagaaaagg 2460
 aaatccataat cttctgttt tgagaagaga gaaatgttagt tgcttactt ccttattcat 2520
 gacagaataa ctgcaaactt ttaagatcag gaaatgtaga catctagtga ttcttttagt 2580
 agacagtttta atttccccca agatttaggag acacttctgt gcaggttcta aaaggagccc 2640
 aatggcctgg ggtggagtg gggagtagat agggatatg tggatggatgg ttaagttca 2700
 tcattggag agttctgttgc tccttgcaag cttagataaa tggatctttt attagatagc 2760
 agtgcatgc ttttaaaaaaa aaaaggcaat gaaaatttag caagccactg aatttgagtt 2820
 ttcaacttgc ttctaatatg ctgtgtgaat cttttttttt ttcttacccct ttcttggct 2880
 taatttcctt actgataaaa tgggttagta atacatcatc caaaaattta ttgcacat 2940
 taaataacat tcctctatgt atctcaatgg cttttttttt tggagatggc aattttgtt 3000
 ggatttgaag ttgagatctt catccaagaa gtagttttc aatttgctag aagcttaatg 3060

Missing mandatory <220> to <223> features to explain "n's" in the sequence. (See next page)

Also see
#10 on the
Error Summary
Sheet.

09/759, 130

p. 20

taggcaagcc acttcatttt tcagaacttg tttactcatt tataatatgg gaataaaaat 3120
tttgtcaagt cagagaaggg tgcttaaaa atgttggc caagccacat gagatcaaag 3180
acacacttt catgacctca aatgtggcc cagcctaggt cagccaaacc ccatccaacc 3240
cttagactca cgaacaatc caccgtagat cagcagagcc accctagatc agctgaaact 3300
ctaagcacaa aaataaaaac ttatcactgt aaaaaaaaaa aaaaaaaaaa aagtctctcg 3360
tatagcaaaa tctaactgtat gcaatctcca tctggccttc atccttctcc cttaattgtc 3420
ctttcgtgta ttgttcatcc agcaaccagg atgatcttgc taaaacatta aacagattct 3480
gtcaykctt maaaaaaaaa aaagccatga aattnagca agccactgaa tttagtttt 3540
cacttgggt tctaataatgc tggtaatc aganagktt tcttaccctt tcttggctt 3600
aatttcctta ctgataaaaat ggggtwgtaa tacctatctc aaaaaattat tgcacatatt 3660
arataacatt cctctatgta tctcaatggc attagacatt aggagaagca ttttggag 3720
gatttgaagt tgagatcttcc atccaagaag tagctttca atttgstaga agcttaatgt 3780
aggcaagcca cttcatttt cagaacttgtt tactcattt ataataatgg aataaaaatt 3840
tgtgcaagtc agagaagggt gccttaaaa ttgttggcc aagccacatg agatcaaaga 3900
cacactttc atgacctcaa atgtggccccc agcctaggtc agccaaacccc catccaaacc 3960
ttagactcac gaacaaatcc acctgagatc agcagagcca ccctagatca gctgaaactc 4020
taagcacaaa aataaaaact tatcactgta aaaaaaaaaa aaaaaaaaaa agaa 4074

This error is indicated elsewhere in the
Sequence listing.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 01/29/2001
PATENT APPLICATION: US/09/759,130 TIME: 13:45:14

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\1759130.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application Number
L:391 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1151 Found:911 SEQ:3
L:578 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1124 Found:884 SEQ:5
L:697 M:252 E: No. of Seq. differs, <211>LENGTH:Input:679 Found:583 SEQ:6
L:706 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:707 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:707 M:252 E: No. of Seq. differs, <211>LENGTH:Input:22 Found:15 SEQ:7
L:771 M:252 E: No. of Seq. differs, <211>LENGTH:Input:423 Found:295 SEQ:8
L:775 M:283 W: Missing Blank Line separator, <400> field identifier
L:776 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:780 M:283 W: Missing Blank Line separator, <400> field identifier
L:781 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:785 M:283 W: Missing Blank Line separator, <400> field identifier
L:786 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (11) SEQUENCE:
L:790 M:283 W: Missing Blank Line separator, <400> field identifier
L:791 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:
L:795 M:283 W: Missing Blank Line separator, <400> field identifier
L:796 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:800 M:283 W: Missing Blank Line separator, <400> field identifier
L:801 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
L:805 M:283 W: Missing Blank Line separator, <400> field identifier
L:806 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:810 M:283 W: Missing Blank Line separator, <400> field identifier
L:811 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:815 M:283 W: Missing Blank Line separator, <400> field identifier
L:816 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:820 M:283 W: Missing Blank Line separator, <400> field identifier
L:821 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:825 M:283 W: Missing Blank Line separator, <400> field identifier
L:826 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:830 M:283 W: Missing Blank Line separator, <400> field identifier
L:831 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:835 M:283 W: Missing Blank Line separator, <400> field identifier
L:836 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (21) SEQUENCE:
L:840 M:283 W: Missing Blank Line separator, <400> field identifier
L:841 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (22) SEQUENCE:
L:845 M:283 W: Missing Blank Line separator, <400> field identifier
L:846 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (23) SEQUENCE:
L:850 M:283 W: Missing Blank Line separator, <400> field identifier
L:851 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (24) SEQUENCE:
L:855 M:283 W: Missing Blank Line separator, <400> field identifier
L:856 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (25) SEQUENCE:
L:860 M:283 W: Missing Blank Line separator, <400> field identifier
L:861 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (26) SEQUENCE:
L:865 M:283 W: Missing Blank Line separator, <400> field identifier
L:866 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (27) SEQUENCE:
L:870 M:283 W: Missing Blank Line separator, <400> field identifier
L:871 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (28) SEQUENCE:

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Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

L:875 M:283 W: Missing Blank Line separator, <400> field identifier
L:876 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (29) SEQUENCE:
L:880 M:283 W: Missing Blank Line separator, <400> field identifier
L:881 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (30) SEQUENCE:
L:1218 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1150 Found:910 SEQ:33
L:1222 M:283 W: Missing Blank Line separator, <400> field identifier
L:1223 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (34) SEQUENCE:
L:1397 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1123 Found:883 SEQ:35
L:1402 M:283 W: Missing Blank Line separator, <400> field identifier
L:1403 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (36) SEQUENCE:
L:1407 M:283 W: Missing Blank Line separator, <400> field identifier
L:1408 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (37) SEQUENCE:
L:1472 M:252 E: No. of Seq. differs, <211>LENGTH:Input:423 Found:295 SEQ:38
L:1476 M:283 W: Missing Blank Line separator, <400> field identifier
L:1477 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (39) SEQUENCE:
L:1811 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1183 Found:1135 SEQ:42
L:1815 M:283 W: Missing Blank Line separator, <400> field identifier
L:1816 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (43) SEQUENCE:
L:1820 M:283 W: Missing Blank Line separator, <400> field identifier
L:1821 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
L:1825 M:283 W: Missing Blank Line separator, <400> field identifier
L:1826 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (45) SEQUENCE:
L:1830 M:283 W: Missing Blank Line separator, <400> field identifier
L:1831 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (46) SEQUENCE:
L:1835 M:283 W: Missing Blank Line separator, <400> field identifier
L:1836 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (47) SEQUENCE:
L:1840 M:283 W: Missing Blank Line separator, <400> field identifier
L:1841 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:
L:1845 M:283 W: Missing Blank Line separator, <400> field identifier
L:1846 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:
L:1850 M:283 W: Missing Blank Line separator, <400> field identifier
L:1851 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (50) SEQUENCE:
L:2260 M:283 W: Missing Blank Line separator, <400> field identifier
L:2261 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (62) SEQUENCE:
L:2265 M:283 W: Missing Blank Line separator, <400> field identifier
L:2266 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (63) SEQUENCE:
L:2270 M:283 W: Missing Blank Line separator, <400> field identifier
L:2271 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (64) SEQUENCE:
L:2275 M:283 W: Missing Blank Line separator, <400> field identifier
L:2276 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (65) SEQUENCE:
L:2280 M:283 W: Missing Blank Line separator, <400> field identifier
L:2281 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (66) SEQUENCE:
L:2285 M:283 W: Missing Blank Line separator, <400> field identifier
L:2286 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (67) SEQUENCE:
L:2290 M:283 W: Missing Blank Line separator, <400> field identifier
L:2291 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (68) SEQUENCE:
L:2295 M:283 W: Missing Blank Line separator, <400> field identifier
L:2296 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (69) SEQUENCE:
L:2300 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY DATE: 01/29/2001
PATENT APPLICATION: US/09/759,130 TIME: 13:45:14

Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

L:2301 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (70) SEQUENCE:
L:2864 M:283 W: Missing Blank Line separator, <400> field identifier
L:2865 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (79) SEQUENCE:
L:2869 M:283 W: Missing Blank Line separator, <400> field identifier
L:2870 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (80) SEQUENCE:
L:2937 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:81
L:2937 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:81
L:2937 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:81
L:2937 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:81
L:2937 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:81
L:2938 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:81
L:2938 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:81
L:2938 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:81
L:2938 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:81
M:340 Repeated in SeqNo=81
L:3107 M:283 W: Missing Blank Line separator, <400> field identifier
L:3108 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (87) SEQUENCE:
L:3155 M:283 W: Missing Blank Line separator, <400> field identifier
L:3156 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (89) SEQUENCE:
L:3160 M:283 W: Missing Blank Line separator, <400> field identifier
L:3161 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (90) SEQUENCE:
L:3227 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:91
L:3227 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:91
L:3227 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:91
L:3227 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:91
L:3227 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:91
L:3228 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:91
L:3228 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:91
L:3228 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:91
L:3228 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:91
M:340 Repeated in SeqNo=91
L:3412 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:96
L:3412 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:96
L:3412 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:96
L:3412 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:96
L:3412 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:96
L:3413 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:96
L:3413 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:96
L:3413 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:96
L:3413 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:96
M:340 Repeated in SeqNo=96
L:3590 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:101
L:3590 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:101
L:3590 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:101
L:3590 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:101
L:3590 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:101
L:3591 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:101
L:3591 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:101
L:3591 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:101

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/759,130
DATE: 01/29/2001
TIME: 13:45:14
Input Set : A:\10147-61.txt
Output Set: N:\CRF3\01292001\I759130.raw

L:3591 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:101
M:340 Repeated in SeqNo=101
L:3764 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:106
L:3764 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:106
L:3764 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:106
L:3764 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:106
L:3764 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:106
L:3765 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:106
L:3765 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:106
L:3765 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:106
L:3765 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:106
M:340 Repeated in SeqNo=106
L:3934 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:111
L:3934 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:111
L:3934 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:111
L:3934 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:111
L:3934 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:111
L:3935 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:111
L:3935 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:111
L:3935 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:111
L:3935 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:111
M:340 Repeated in SeqNo=111
L:4037 M:283 W: Missing Blank Line separator, <400> field identifier
L:4038 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (116) SEQUENCE:
L:4042 M:283 W: Missing Blank Line separator, <400> field identifier
L:4043 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (117) SEQUENCE:
L:9098 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:9099 M:252 E: No. of Seq. differs, <211>LENGTH:Input:24 Found:15 SEQ:300
L:9617 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:324
L:9617 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:324
L:9617 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:324
L:10982 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:343
L:16673 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:450
L:16720 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:451
L:16752 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:452
L:16778 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:453
L:16805 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:454
M:340 Repeated in SeqNo=454
L:16831 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:455
L:16852 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:456
M:340 Repeated in SeqNo=456
L:16893 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:457
M:340 Repeated in SeqNo=457